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Copyright (c) 1993 - 2000 Comp
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sp_vertebrate:*
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176.5	179	182.5	187	189.5	212	222.5	234.5	237.5	243	249	251	261.5	266	268.5	270.5	277.5	278	279	283	284	284.5	294.5	294.5	328	328
7.3	7.4	7.5	7.7	7.8	8.7	9.2	9.7	9.8	10.0	10.3	10.3	10.8	11.0	11.1	11.1	11.4	11.5	11.5	11.7	11.7	11.7	12.1	12.1	13.5	13.5
77	267	75	268	88	95	112	121	104	122	124	124	102	150	121	131	116	118	122	112	118	113	298	119	147	116
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075741	Q90529	075743	Q90524	075737	Q9ULB6	Q9UGP3	Q9UL96	Q9UL87	Q9UL75	Q9N0W4	Q9N0W6	Q9JL79	095973	Q9UL71	Q9UL88	Q9UL93	Q9UL91	Q9UL84	Q9HCC1	Q9UL72	Q9UL90	Q9QYF0	Q9UL73	Q9Y509	Q9UL89
075741 homo sapien	Q90529 ginglymosto	075743 homo sapien	Q90524 ginglymosto	075737 homo sapien	homo	homo	homo	Q9ul87 homo sapien	Q9u175 homo sapien	Q9n0w4 oryctolagus	Q9n0w6 oryctolagus	Q9j179 mus musculu	homo	Q9u171 homo sapien	homo	homo	homo	homo	Q9hcc1 homo sapien	Q9u172 homo sapien	Q9u190 homo sapien	Q9qyf0 mus musculu	homo	homo	Q9u189 homo sapien

## ALIGNMENTS

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EX SEQUENCE FROM N.A.

RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

RT Cloning of cDNAs encoding for anti-white pine blister rust monoclonal RT antibody (Mab 7, its light and heavy chains) and construction of a RT single Chain antibody (ScTV).";

RI Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF152372; AAD40243.1; --

DR HSSP; P01842; 7FAB.

DR InterPro; IPR003006; -.

DR InterPro; IPR003500; -.

DR Pfam; PF00047; ig; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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Best Local Similarity
Matches 275; Conserv
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Q9R1A4;
Q1-MAY-2000
01-MAY-2000
01-MAY-2001
01-MAR-2001
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NON_TER
SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TREMBLREL. 16, Last annotation update)
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
60
                               57 GSIFSPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYYFDYWGQGTTLTV 116
                                                                                 2 VQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWI-----GGINPYYG
                                                              1 VQLQESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASFSSGGI-IYYT 59
DSV-----KGRFTIYKDKDRNILSLQMSSLRSEDTAMYYCAR---GDYSAYWGPGTLVTV 111
                                                                                                                                                                                                                  437
437 AA;
                                                                                                                                Conservative
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                                                                                                                               58.8%; Score 1426; DB 11; 60.0%; Pred. No. 1.5e-104; tive 63; Mismatches 94;
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Best Local
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Interpro; IPRO03596; -.
Pfam; PF00047; ig; 4.
PROSITE; PS00290; IG_MHC;
SMART; SM00406; IGV; 1.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat.
IMMUNOGLOBULIN HEAVY CHAIN VARIANT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
EMBL; AL389978; CAB97534.1; -
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Lehrach H., Poustka A., Lundeberg J
"The European IMAGE consortium for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pluvinet R., Estivill X., Escarceller M., Sumo Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                         158
                                                                                                                           102
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                                                                          59
                                                                                                                                                                                                                                                                        Local Similarity
mes 143; Conserv
                                                                                                                                                                           N
                    TWNSGSLSSSVHTFPALLQSG--LYTMSSSVTVPSSTWP-SQTVTCSVAH---
                                                                                            AYY-FDYWGQGTTLTVSSAKTTPPSYYPLAPGCGDTT--GSSVTLGCLVKGYFP-ESVTV 157
                                                                                                                                                                                                                    GESLEWIGGINPYYGGSIFSPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAG 101
                                                                     TYYGMDVWGQGTTVTVSSASPTSPKVFPLSL---DSTPQDGNVVVACLVQGFFPQEPLSV 115
                                                                                                                                                                      GKGLEWVSRISSSGDTVDYADSVKGRFTVSRDTAKNSLSLQMSSLRVEDTAVYYCAR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVPEVS----SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQT
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                                                                                                                                                                                                                                                                                                                                                                                                   416 AA; 44786 MW;
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG_MHC; UNKNOWN_2
                                                                                                                                                                                                                                                                                                 22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ballabio A.,
                                                                                                                                                                                                                                                                     ; Score 543; DB 4; Lo; Pred. No. 6.3e-35; 76; Mismatches 162;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   8C41708BB8AB4687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            integrated Molecular analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Estivill
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DBJ databases
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                                                                                                                                                                                                                                                                                                                   Length 416;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gibson K.,
                                                                                                                                                                                                                                                                        48;
                 PASSTTV 211
                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                         58
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RESULT
Q9UP60
ID Q9
AC Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
DT 01
DT SN
GN SN
GN SN
GN SN
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Q9QXF0
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Best Local :
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                                                                                                         Q9UP60;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9QXFO
O9QXFO
O9QXFO
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemens A., Rademaekers A., submitted (DEC-1997) to the EMBL; AJ225171; CAB65236.1;
                                                          SNC73
                                                                                   SNC73 PROTEIN.
                                                                                                                                                                                                                      Q9UP60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390
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                                                                                                                                                                                                                                                                                                                                                      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAYYYCARDKD-YYFDYWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                           SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYYFDYWGQGTTLTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPELKTPLTANITK-SGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GL-RDASGATFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAQPWNHGETFTCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
117 AA;
                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---CPVPPPPPC--CH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13060 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.8%;
                                                                                                            13,
13,
16,
                                                                                                            Last sequence update)
Last annotation updat
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                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 480.5; DB 1
Pred. No. 1.1e-30;
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D816AD0858A47E4C
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                                                                                                                                                                                                                      A
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                                                                                                            update)
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                                                                                                                                                                                                                                                                                                                                                                                                           118
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Eukaryota; Metazoa; Homo sapiens (Human)

Chordata; Craniata; Vertebrata;

Euteleostomi;

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RESULT Q90XE9
ID Q9
ID Q9
AC Q9
AC Q9
DT 01
DT 0
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Best Local Similarity
Matches 130; Conserv
                  Clemens A., Rademaekers A., Submitted (DEC-1997) to the EMBL; AJZ25174; CAB65237.1; InterPro; IPR003006; -. InterPro; IPR003596; -.
                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                            Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
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Zheng S., Cao J., Cao W., Cai X., Geng L.;

Zheng S., Cao J., Cao W., Cai X., Geng L.;

"Identification and characterization of SNC73, a gene wiregulated in colorectal cancer.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 Q9QXE9;
                                                                                                                                                                                                                                                                                                                                                                                                                           Q9QXE9
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InterPro; IPR003507; -.
Pfam; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SMART; SM00407; IGC1; 1.
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLVVGFNPGDISVEWTSNGH--TEENYKDTAPVLD-SDG--SYFIYSKLNMKTSKWEKTD
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                                                                                                                                                                                                                      ; Chordata; Rodentia;
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                                                                                             Specht C., Koelsch EMBL/GenBank/DDBJ c
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Pred. No. 1.9e-29;
0; Mismatches 152;
                                                                                                                                                                                                                 Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catarrhini; Hominidae;
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PARTITION OF THE PARTIT
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Best L
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Best Local
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Q9Z1C4;
Q9Z1C4;
01-MAY-1999
01-MAY-1999
01-MAR-2001
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE RE
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalla; Eutheria; Rodentia; Sciurognathi; Murid
NCBI_TaxID-10090;
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NON_TER
SEQUENCE
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STRAIN-BALB/C;

Malklel S., Liao L., Cunningham M.W., Diamond B.;

"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditi.

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF206031; AAF69329.1; ...
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SEQUENCE
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01-OCT-2000
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON_TER 1
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REG
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01-MAR-2001
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90; Conservative
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                                                                                                                                                                                                         PRELIMINARY;
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12118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.1%;
73.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13000 MW;
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75.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 414; DB 11; L
Pred. No. 1.7e-25;
Pred. No. 1.7e-25; 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 458.5;
Pred. No. 5.9e
11; Mismatches
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Craniata; Vertebrata; Sciurognathi; Muridae;

Muridae;

Euteleostomi; Murinae;

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SEQUENCE
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF206025; AAF69323.1; -
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SMART; SM00406; IGv; 1.
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SEQUENCE FROM N.A.
STRAIN-BALB/C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Humanized porcine VCAM-specific monoclonal antibodies IgG2/G4 constant regions block human leukocyte binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matis L.M., Evans M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mueller J.P.,
                                                                                                                                                                                                                                                                                                                                                                                               nterPro; IPR003006; -.
                      69
                                                                                                                                                    Local Similarity 66.7 hes 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                    TLTVDKSSSTAYMELRSLTSEDSAVYYCARR----AGAYYFDYWGQGTTLTVSS
                                                                                           PELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIFSPKFKGKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGYFDYWGQGTTLTVSS
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PQLVRPGASVKISCKASGYSFTSYWMHWVKQRPGQGLEWIGMIDPSDSETRLNQKFKDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U78801; AAD00293.1; -.
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                                                                                                                                                                                                                                                                 114 AA;
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; 13036 MW;
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12829 MW;
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, Last annotation update)
HEAVY CHAIN VARIABLE REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 401; DB 1
Pred. No. 2e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi;
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                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
                                                                                                                                                                           DB 11;
.6e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Q90544 PRELIMINARY; PRT; 68
Q90544;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequer
01-MAR-2001 (TrEMBLrel. 16, Last annote
NOVEL ANTIGEN RECEPTOR PRECURSOR.
Ginglymostoma cirratum (Nurse shark)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JL77
Q9JL77
                                         EMBL; U18701; AAB48195.1; HSSP; P01857; 1FC1.
                                                                                                                                Nature 374:168-173(1995).
                                                                                                                                                                                                                            Greenberg A.S.,
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii, Galeomorphii; Galeoidea; Orectolobiformes;
                                                                                                                                                                                                                                                    MEDLINE=95183140;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                         Ginglymostomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrembLrel. 15, 01-OCT-2000 (TrembLrel. 15, 01-MAR-2001 (TrembLrel. 16, ANTI-MYOSIN IMMUNOGLOBULIN )
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7801;
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SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                   InterPro;
                                                                                                                                                                              'A new antigen receptor gene family that undergoes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
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                                                                                         DOMAIN
                                                                                                               SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                   IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003006; -. IPR003596; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 AA;
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                                                                                                                                                                                                                                                                                                  N.A.
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                                                                                                                                                                                                                               Avila
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                                                                                                               IMMUNOGLOBULIN
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.6%;
65.7%;
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                                                                                                                                                                                                                               D.,
                                                                                                                                                                                                                               Hughes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Last sequence update)
, Last annotation update)
HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation
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Pred. No. 1e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence update)
                                                                                                               AND
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                                                                                                                                                                                                                               Hughes A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       684
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                                                                                                               HISTOCOMPATIBILITY COMPLEX
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SMART; PROSITE;

SM00407;

IGc1;

PF00047; ig; 6. TE; PS00290; IG\_MHC;

UNKNOWN\_3

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RESULT
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Best Local :
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SEQUENCE FROM N.A.
MEDLING-98322155; PubMed-9657749;
Jacquemin M.G., Vander Elst L.P.L.;
Mechanism and kinetics of factor V
IgG4 monoclonal antibody derived fr
                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                  01-NOY-1999 (TrEMBLrel. 12, Created)
01-NOY-1999 (TrEMBLrel. 12, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
IGG VH PROTEIN PRECURSOR (FRAGMENT).
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Pred. No. 3.
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                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
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095978;
01-MAY-1999
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SEQUENCE
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SIGNAL
                                                                                                                                                             "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated w somatic mutations within the unslated regions of rearranged class switch recombinated Ig genes.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Blood 92:496-506(1998).
                                                                                                 SMART; SM00406;
                                                                                                           InterPro; IPR003596; -. Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                           Jox A., Zander T., Kueppers R., Irsch J., Bohlen H., Diehl V., Wolf J.;
                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ224083; CAA11829.1;
                                                                                                                                           EMBL; AJ005570; CAA06599.1;
                                                                                                                                                                                                                                                  TISSUE-PERIPHERAL BLOOD;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       VH1 PROTEIN
                                                                                                                               InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYYFDYWGQGTTLTVSSAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              TKGPSVFPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTPPSVYPL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA-VPDPDAFDIWGQGTMVTVSSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00406;
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              Similarity
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157
157
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nilarity 56.6%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 /
                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 16, Last annotation updat
PRECURSOR (FRAGMENT).
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                         AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                 IGV; 1
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                                                        21
157
17304
15.2%; Pre
51.9%; Pre
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16031 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
                                                         MW:
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                                                                                                                                           .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 371.5; D
Pred. No. 5.9e-
18; Mismatches
   Score 369.5; DB 4;
Pred. No. 8.9e-22;
Pred. No. 8.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                         86986EDDA84D88B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563D164AB22802D5
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                                                                                                                                                                                                                                                                                                                                                                                           157
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                                                                                                                                                                                                                                        Kanzler
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     Indels
                        Length
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    5;
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                                                                                                                                                                 COMPLEX
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RESULT
Q9UL92
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Best Local S
Matches 72
                                                                                                                   (1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                   Q9UL92
Q9UL92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9GYZ2;
Q9GYZ2;
                                     Clin.
                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
SUBL; AF282622; AAG01452.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora;
Trematoda; Digenea; Strigeidida; Schistosomatoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TIEMBLIEL. 16, Created)
01-MAR-2001 (TIEMBLIEL. 16, Last sequence update)
01-MAR-2001 (TIEMBLIEL. 16, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN
                                                            fetus.";
                                                                                                        Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Song X.T., Feng Z.Q., Guan X.H.;
"Amplification, cloning and sequence
"variable region gene of monoclonal ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                  Myosin-reactive autoantibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
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                    SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSSTKGPSVFPLAP 153
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                                            Immunol
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                 Immunopathol. 87:18
TO IMMUNOGLOBULIN
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                                                                                                                                                                                                                                Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 366.5; DB 5;
Pred. No. 1.1e-21;
                                        87:184-192(1998)
                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                    AND MAJOR
                                                                                rheumatic
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                                                                                                                          Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                         124
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                    HISTOCOMPATIBILITY COMPLEX
                                                                                  carditis
                                                                                                                          Berney
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                                                                                                                                                                                                                                                                                                 REGION (FRAGMENT).
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Schistosomatidae;
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Q9JL85
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Best Local S
Matches 69
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Best Local
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InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
NON TER 1
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Q9JL85;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REG
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autolamune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF206021; AAF69319.1;
InterPro; IPR003006; -.
InterPro; IPR003596; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 LYTYSS
  62
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ELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIFSPKFKGKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR--GLYVVVPAAFSRFDYWGQGT
                                                                                                ELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60
                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 56.371; Conservative
                                                                                                                                                                                                                                                                                                                     109
109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124
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                                                                                                                                                                                              Conservative
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13580
                                                                                                                                                                                                                                                                                                                        11944 MW;
                                                                                                                                                                                                                14.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW.
                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                              Score 358.5; DB 1
Pred. No. 4.1e-21;
3; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 364;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                        DFE615FE6CED4EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
.8e-21;
                                                                                                                                                                                                                                              DB 11;
                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGION
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                              Length
     109
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                                                                                                                                                                                                                                                   109;
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                                                                                                                                                                                                1;
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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June 18,

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